SEQUENCE LISTING

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      Tang, Liang
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<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND
      CANINE IL-13 RECEPTORS

<130> AL-7

<140> not yet assigned
<141> 2001-04-09

<150> 60/195,659
<151> 2000-04-07

<150> 60/195,874
<151> 2000-04-07

<160> 104

<170> PatentIn Ver. 2.1

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<220>
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 1   5   10   15

cct   51
Pro

<210> 2
<211> 17
<212> PRT
<213> Canis familiaris

<400> 2

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 1   5   10   15

Pro

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<211> 51
<212> DNA
<213> Canis familiaris

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<211> 1654
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<213> Canis familiaris

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<222> (70)..(1473)

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gacaccacc atg gag tct gtg ttc tgc tgg gtt ttc ctt gtc gtt att tta 111
          Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu
           1   5   10

aaa ggt gtc cag ggt gag gtg cag ttg gtg gag tct ggg gga gac ctg   159
Lys Gly Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
 15   20   25   30

gtg aag cct ggg ggg tcc ctg aga ctc tcc tgt gtg gcc tct gga ttc   207
Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
                35   40   45

acc ttc agt tcg tac tac atg cat tgg atc cgc cag gct cca ggg aag   255
Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys
            50   55   60

ggg ctt cag cgg gtc gca cat att aga ggt gat gga agg act aca cac   303
Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His
            65   70   75

2

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tac gca gac gct atg aag ggc cga ttc acc atc tcc aga gac aac gcc      351
Tyr Ala Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
        80                  85                  90

aag aac acg ctg tat ctg cag atg aat agc ctg aca gtc gaa gac acg      399
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr
 95                     100                 105                 110

gct att tat tac tgt gta aag gac ata tac tat ggg gtc ggg gac tat      447
Ala Ile Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr
                115                 120                 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc      495
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala
            130                 135                 140

ccc tcg gtt ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc      543
Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
            145                 150                 155

acg gtg gcc ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta      591
Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
        160                 165                 170

act gtg tcc tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc      639
Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
175                 180                 185                 190

ccg tcc gtc ctg cag tcc tca ggg ctt cac tcc ctc agc agc atg gtg      687
Pro Ser Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val
                195                 200                 205

aca gtg ccc tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg      735
Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
                210                 215                 220

gtc cac cca gcc agc aac act aaa gta gac aag cca gtg ttc aat gaa      783
Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu
        225                 230                 235

tgc aga tgc act gat aca ccc cca tgc cca gtc cct gaa cct ctg gga      831
Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly
        240                 245                 250

ggg cct tcg gtc ctc atc ttt ccc ccg aaa ccc aag gac atc ctc agg      879
Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
255                 260                 265                 270
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3

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att acc cga aca ccc gag gtc acc tgt gtg gtg tta gat ctg ggc cgt      927
Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg
            275             280             285

gag gac cct gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg      975
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
            290             295             300

cac aca gcc aag acc cag tct cgt gag cag cag ttc aac ggc acc tac     1023
His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr
            305             310             315

cgt gtg gtc agc gtc ctc ccc att gag cac cag gac tgg ctc aca ggg     1071
Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
            320             325             330

aag gag ttc aag tgc aga gtc aac cac ata gac ctc ccg tct ccc atc     1119
Lys Glu Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile
335             340             345             350

gag agg acc atc tct aag gcc aga ggg agg gcc cat aag ccc agt gtg     1167
Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val
            355             360             365

tat gtc ctg ccg cca tcc cca aag gag ttg tca tcc agt gac aca gtc     1215
Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
            370             375             380

agc atc acc tgc ctg ata aaa gac ttc tac cca cct gac att gat gtg     1263
Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val
            385             390             395

gag tgg cag agc aat gga cag cag gag ccc gag agg aag cac cgc atg     1311
Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met
            400             405             410

acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag     1359
Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
415             420             425             430

ctc tct gtg gac aag agc cgc tgg cag cag gga gac ccc ttc aca tgt     1407
Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys
            435             440             445

gcg gtg atg cat gaa act cta cag aac cac tac aca gat cta tcc ctc     1455
Ala Val Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
            450             455             460
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4

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tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc          1503
Ser His Ser Pro Gly Lys
        465


cccacccttg gctctcagga tcccctgagg acacctgagc ccctgtccct gtgtacataa 1563

ccctgggtag gcacccatca tgaaataaag cacccagcac tgccctgggc cctgcaaaaa 1623

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                                 1654



<210> 5
<211> 468
<212> PRT
<213> Canis familiaris

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  1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
             20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
         35                  40                  45

Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
     50                  55                  60

Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala
 65                  70                  75                  80

Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                 85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile
            100                 105                 110

Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly
            115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser
        130                 135                 140

Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val
145                 150                 155                 160
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5

Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val
            165   170   175

Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser
            180   185   190

Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val
            195   200   205

Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
    210   215   220

Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg
225   230   235   240

Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro
                245   250   255

Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr
            260   265   270

Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp
    275   280   285

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr
    290   295   300

Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val
305   310   315   320

Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu
            325   330   335

Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg
            340   345   350

Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val
            355   360   365

Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile
    370   375   380

Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
385   390   395   400

Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro
                405   410   415

6

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Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser
        420                     425                 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val
        435                     440                 445

Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His
    450                     455                 460

Ser Pro Gly Lys
465
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<212> DNA
<213> Canis familiaris

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tcctcagggg atcctgagag ccaagggtgg ggggcttgct gggtgccggg cgtgttgctc 180
atttacccgg agaatgggag agggatagat ctgtgtagtg gttctgtaga gtttcatgca 240
tcaccgcaca tgtgaagggg tctccctgct gccagcggct cttgtccaca gagagcttgc 300
tgtacaggaa gtaggacccg tcctcgtcca gctggggcgg ggtcatgcgg tgcttcctct 360
cgggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg tagaagtctt 420
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gagacgggag gtctatgtgg ttgactctgc acttgaactc cttccctgtg agccagtcct 600
ggtgctcaat ggggaggacg ctgaccacac ggtaggtgcc gttgaactgc tgctcacgag 660
actgggtctt ggctgtgtgc acctccttac catccacgaa ccagctgatc tgcacctcag 720
ggtcctcacg gcccagatct aacaccacac aggtgacctc gggtgttcgg gtaatcctga 780
ggatgtcctt gggtttcggg ggaaagatga ggaccgaagg ccctcccaga ggttcaggga 840
ctgggcatgg gggtgtatca gtgcatctgc attcattgaa cactggcttg tctactttag 900
tgttgctggc tgggtggacc acgttgcagg tgaaggtctc gctgggccac ctgctggagg 960
gcactgtcac catgctgctg agggagtgaa gccctgagga ctgcaggacg gacgggaagg 1020
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agcctgacac caggcaggcc agggccaccg tggagccgga agtggacccg cagctggggg 1140
ccagtgggaa aaccgagggg gccgtggtgg aggctgagga cggtgacc agggttccct 1200
ggccccaata gtccccgacc ccatagtata tgtcctttac acagtaataa atagccgtgt 1260
cttcgactgt caggctattc atctgcagat acagcgtgtt cttggcgttg tctctggaga 1320
tggtgaatcg gcccttcata gcgtctgcgt agtgtgtagt ccttccatca cctctaatat 1380
gtgcgacccg ctgaagcccc ttccctggag cctggcggat ccaatgcatg tagtacgaac 1440
tgaaggtgaa tccagaggcc acacaggaga gtctcaggga ccccccaggc ttcaccaggt 1500
ctcccccaga ctccaccaac tgcacctcac cctggacacc ttttaaaata acgacaagga 1560
aaacccagca gaacacagac tccatggtgg tgtctgtgtt gtgtcctgag cactgaatgg 1620
ggtcacctgg ggatcctggg ggctggctcg tgcc                             1654
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7

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<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(51)

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Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
  1   5   10   15

tca   51
Ser

<210> 8
<211> 17
<212> PRT
<213> Canis familiaris

<400> 8
Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
  1   5   10   15

Ser

<210> 9
<211> 51
<212> DNA
<213> Canis familiaris

<400> 9
tgattcaggg actgggcatg gggatataca cttgcaggtg gactctttgg g   51

<210> 10
<211> 1460
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (48)..(1457)

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                                                     Met Glu Ser
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gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt   104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
         5   10   15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg   152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 20   25   30   35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat   200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                     40   45   50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc   248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
                 55   60   65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag   296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
             70   75   80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc   344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
         85   90   95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg   392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
100   105   110   115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat   440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                 120   125   130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt   488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
                 135   140   145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc   536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
             150   155   160

9

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ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc     584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
    165                 170                 175

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc     632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
180                 185                 190                 195

ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc     680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro
                200                 205                 210

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg     728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro
            215                 220                 225

gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc     776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys
            230                 235                 240

aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg     824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser
    245                 250                 255

gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga     872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg
260                 265                 270                 275

aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct     920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro
                280                 285                 290

gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc     968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala
            295                 300                 305

aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc    1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val
            310                 315                 320

agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc    1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe
    325                 330                 335

aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act    1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr
340                 345                 350                 355
```

10

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atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg      1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
                360                 365                 370

cca cca tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc      1208
Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr
                375                 380                 385

tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag      1256
Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
            390                 395                 400

agc aat gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc      1304
Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro
        405                 410                 415

cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg      1352
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
420                 425                 430                 435

gac aag agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg      1400
Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met
                440                 445                 450

cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct      1448
His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser
                455                 460                 465

ccg ggt aaa tga                                                       1460
Pro Gly Lys
        470



<210> 11
<211> 470
<212> PRT
<213> Canis familiaris

<400> 11
Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly
  1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
            35                  40                  45
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11

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Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
    50                      55                  60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
65                      70                  75                  80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
                85                  90                  95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
                100                 105                 110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
            115                 120                 125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
145                 150                 155                 160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
                165                 170                 175

Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
                180                 185                 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
            195                 200                 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
    210                 215                 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225                 230                 235                 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
                260                 265                 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
                275                 280                 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
    290                 295                 300
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```
His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
305             310             315                 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
                325             330             335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile
            340             345             350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
            355             360             365

Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
        370             375             380

Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val
385             390             395                 400

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr
                405             410             415

Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
            420             425             430

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys
            435             440             445

Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
        450             455             460

Ser His Ser Pro Gly Lys
465             470


<210> 12
<211> 1460
<212> DNA
<213> Canis familiaris

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gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg gaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300
caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
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13

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ggggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc  420
ctggtgctca atggggagga cgctgaccac acggtaggtg ctgttgaact gctgctcacg  480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc  540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct  600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg  660
gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt  720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga  780
gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa  840
ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag gctcggggaa  900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg  960
ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc  1020
attgccccag tggtccatac cataataatg tcgcggccat actcccgtca cacagtgata  1080
gattgccgtg tcctcggctt tcaggctgct catctggaga tacagcgtgt tcttggcgtt  1140
gtctctggag atggtgaatc ggcccttcac agcgtctgcg tagtaagtat ctccacgatt  1200
gctaacagct gcgacccact gcagccccct ccctggagac tgacggaccc aactcatgcc  1260
atagtcactg aaggtgaatc cagaggccac acaggacagt ctcaaggacc ccccaggctt  1320
caccaggtct cccccagact ccaccagttg cacctcaccc tggacacctt ttaaaataga  1380
gacaaggaaa acccagcaga gcacagactc catggtggtt tgtctgtgtt gtgtcctgag  1440
cactgaatgg ggtcacctgg                                                 1460


<210> 13
<211> 60
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(60)

<400> 13
gcc aaa gaa tgc gag tgc aag tgt aac tgt aac aac tgc cca tgc cca   48
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
 1               5                  10                  15

ggt tgt ggc ctg                                                   60
Gly Cys Gly Leu
            20



<210> 14
<211> 20
<212> PRT
<213> Canis familiaris

<400> 14
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
 1               5                  10                  15
```

14

Gly Cys Gly Leu
                20

<210> 15
<211> 60
<212> DNA
<213> Canis familiaris

<400> 15
caggccacaa cctgggcatg ggcagttgtt acagttacac ttgcactcgc attctttggc 60

<210> 16
<211> 1456
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1453)

<220>
<223> At location 27, n = unknown

<400> 16
aagtgctcag gcacaacaca gacaaancac c atg gag tct gtg ctc tac tgg   52
                                   Met Glu Ser Val Leu Tyr Trp
                                    1   5

gtt ttc ctt gtc gct att tta aag ggt gtc cag ggt gac gtg cag ctg   100
Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu
         10   15   20

gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg   148
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu
     25   30   35

tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg   196
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp
  40   45   50   55

gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg   244
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg
                 60   65   70

15

```
tat gat gga agt gat ata tac tac gca gac gct gtg aag ggc cga ttc      292
Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala Asp Ala Val Lys Gly Arg Phe
                75                  80                  85


agc atc tcc aga gac aac gcc aag aac acg gtg tat ctg cag atg aac      340
Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn
                90                  95                  100


agc ctg aga gcc gag gac acg gcc gtg tat tat tgt gcg aag gcc ccc      388
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ala Pro
    105                 110                 115


ccc tac gat agt tac cac tat ggt atg gac tat tgg ggt cct ggc act      436
Pro Tyr Asp Ser Tyr His Tyr Gly Met Asp Tyr Trp Gly Pro Gly Thr
120                 125                 130                 135


tcc ctc ttc gtg tcg tca gcc tcc acc acg gcc ccc tcg gtt ttc cca      484
Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro
                140                 145                 150


ctg gcc ccc agc tgt ggg tcc caa tcc ggc tcc acg gtg gcc ctg gcc      532
Leu Ala Pro Ser Cys Gly Ser Gln Ser Gly Ser Thr Val Ala Leu Ala
                155                 160                 165


tgc ctg gtg tca ggc tac atc ccc gag cct gta act gtg tcc tgg aat      580
Cys Leu Val Ser Gly Tyr Ile Pro Glu Pro Val Thr Val Ser Trp Asn
                170                 175                 180


tcc gtc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag      628
Ser Val Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln
    185                 190                 195


tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc      676
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser
200                 205                 210                 215


agg tgg ccc agc gag acc ttc acc tgc aat gtg gcc cac ccg gcc acc      724
Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Thr
                220                 225                 230


aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt      772
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                235                 240                 245


aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct      820
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
    250                 255                 260
```

16

```
tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc      868
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
    265                 270                 275

cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac      916
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
280                 285                 290                 295

cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca      964
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
                300                 305                 310

gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg     1012
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
            315                 320                 325

gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag     1060
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
        330                 335                 340

ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag     1108
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
        345                 350                 355

atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc     1156
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
360                 365                 370                 375

ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc     1204
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
            380                 385                 390

tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag     1252
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
            395                 400                 405

agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc     1300
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
            410                 415                 420

cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg     1348
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
    425                 430                 435

gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg     1396
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
440                 445                 450                 455
```

17

```
cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct       1444
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
                460                 465                 470

ccg ggt aaa tga                                                        1456
Pro Gly Lys


<210> 17
<211> 474
<212> PRT
<213> Canis familiaris
<223> At location 27, n = unknown

<400> 17
Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly
 1               5                  10                  15

Val Gln Gly Asp Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
                20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
             35                  40                  45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Pro
     50                  55                  60

Gln Trp Val Ala Thr Ile Arg Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala
 65                  70                  75                  80

Asp Ala Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn
                 85                  90                  95

Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
                100                 105                 110

Tyr Tyr Cys Ala Lys Ala Pro Pro Tyr Asp Ser Tyr His Tyr Gly Met
            115                 120                 125

Asp Tyr Trp Gly Pro Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr
    130                 135                 140

Thr Ala Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Gln Ser
145                 150                 155                 160

Gly Ser Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Ile Pro Glu
                165                 170                 175
```

18

Pro Val Thr Val Ser Trp Asn Ser Val Ser Leu Thr Ser Gly Val His
        180   185   190

Thr Phe Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195   200   205

Met Val Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys
    210   215   220

Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Pro Val Ala
225   230   235   240

Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro Gly
        245   250   255

Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
        260   265   270

Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val Thr Cys Val Val
        275   280   285

Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile Ser Trp Phe Val
    290   295   300

Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro Arg Glu Glu Gln
305   310   315   320

Ser Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln
            325   330   335

Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val Asn Asn Lys Ala
        340   345   350

Leu Pro Ser Pro Ile Glu Glu Ile Ile Ser Lys Thr Pro Gly Gln Ala
        355   360   365

His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Met Ser
    370   375   380

Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp Phe Phe Pro Pro
385   390   395   400

Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser
            405   410   415

Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe
        420   425   430

19

Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp
        435   440   445

Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
    450   455   460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys
465   470

<210> 18
<211> 1456
<212> DNA
<213> Canis familiaris

<220>
<223> At location 1430, n = unknown

<400> 18
tcatttaccc ggagaatggg agagggatat ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcag 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg agatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgtc 720
tactttagtg ttggtggccg ggtgggccac attgcaggtg aaggtctcgc tgggccacct 780
gctggagggc actgtcacca tgctgctgag ggagtagagc cctgaggact gcaggacgga 840
cgggaaggtg tgcacaccgc tggtcaagga gacggaattc caggacacag ttacaggctc 900
ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggacccaca 960
gctggggggcc agtgggaaaa ccgaggggggc cgtggtggag gctgacgaca cgaagaggga 1020
agtgccagga ccccaatagt ccataccata gtggtaacta tcgtaggggg gggccttcgc 1080
acaataatac acggccgtgt cctcggctct caggctgttc atctgcagat acaccgtgtt 1140
cttggcgttg tctctggaga tgctgaatcg gcccttcaca gcgtctgcgt agtatatatc 1200
acttccatca taccgaatag ttgcgaccca ctgaggcccc ttccctggag actgacggac 1260
ccagctcatg gcacagctac taaaggtgaa tccagaggcc acacaggaca gtctcaagga 1320
cccccccaggc ttcaccaggt ctcccccaga ctccaccagc tgcacgtcac cctggacacc 1380
ctttaaaata gcgacaagga aaacccagta gagcacagac tccatggtgn tttgtctgtg 1440
ttgtgcctga gcactt 1456

<210> 19

20

<211> 1453
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1450)

<400> 19
agtgctcagg acaccacaca gacaaatcac c atg gag tct gtg ctc ttc tgg   52
                                            Met Glu Ser Val Leu Phe Trp
                                              1   5

gtt ttc ctt gtc act att tta aaa ggt gtc cag ggt gag gta cgt ttg   100
Val Phe Leu Val Thr Ile Leu Lys Gly Val Gln Gly Glu Val Arg Leu
        10   15   20

gtg gag tct gga gga acc ctg gtg aag cct ggg ggg tcc ctg aaa ctc   148
Val Glu Ser Gly Gly Thr Leu Val Lys Pro Gly Gly Ser Leu Lys Leu
    25   30   35

tct tgt gtg gcc tct gga ttc acc ttc aga aga tac tcc atg gac tgg   196
Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr Ser Met Asp Trp
   40   45   50   55

gtc cgc cag gct cca ggc aag agc ctg cag tgg gtc gcc ggg att aac   244
Val Arg Gln Ala Pro Gly Lys Ser Leu Gln Trp Val Ala Gly Ile Asn
                60   65   70

ggt gat ggc aca gga aca tcc tat tca cag act gtg aag ggc cga ttc   292
Gly Asp Gly Thr Gly Thr Ser Tyr Ser Gln Thr Val Lys Gly Arg Phe
                75   80   85

acc atc tcc aga gac aac gcc aag aac acc ctc tat ctg cag ata aac   340
Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Ile Asn
            90   95   100

agc ctg aga gcc gaa gac tct gct gtg tat tat tgt gcc aag agc tgg   388
Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Ser Trp
    105   110   115

tct cgt aat ggg gat ctt gac tac tgg ggc cag gga acc ctg gtc acc   436
Ser Arg Asn Gly Asp Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
120   125   130   135

gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg gcc ccc   484
Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro
            140   145   150

21

agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc ctg gtg   532
Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys Leu Val
            155   160   165

tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc ggc tcc   580
Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ser
            170   175   180

ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc tca ggg   628
Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser Ser Gly
        185   190   195

ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc agg tgg ccc   676
Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser Arg Trp Pro
200   205   210   215

agc gag acc ttc acc tgc aac gtg gcc cac ccg gcc agc aaa act aaa   724
Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Ser Lys Thr Lys
                220   225   230

gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt cct cgc cca   772
Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro
            235   240   245

cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga ggg cct tcg   820
Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser
            250   255   260

gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg att gcc cga   868
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg
        265   270   275

aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca gaa gac cct   916
Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro
280   285   290   295

gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg caa aca gcc   964
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala
                300   305   310

aag act cag cct cgt gag gag cag ttc aat ggc acc tac cgt gtg gtc   1012
Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr Arg Val Val
            315   320   325

agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg aag cag ttc   1060
Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe
            330   335   340

22

acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc   1108
Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr
    345   350   355

atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg   1156
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
360   365   370   375

ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc   1204
Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys
          380   385   390

ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc   1252
Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser
          395   400   405

aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag   1300
Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln
        410   415   420

ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac   1348
Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp
        425   430   435

aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat   1396
Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His
440   445   450   455

gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg   1444
Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro
          460   465   470

ggt aaa tga   1453
Gly Lys

<210> 20
<211> 473
<212> PRT
<213> Canis familiaris

<400> 20
Met Glu Ser Val Leu Phe Trp Val Phe Leu Val Thr Ile Leu Lys Gly
  1   5   10   15

Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys
        20   25   30

23

Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
        35   40   45

Arg Arg Tyr Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Ser Leu
        50   55   60

Gln Trp Val Ala Gly Ile Asn Gly Asp Gly Thr Gly Thr Ser Tyr Ser
65   70   75   80

Gln Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
            85   90   95

Thr Leu Tyr Leu Gln Ile Asn Ser Leu Arg Ala Glu Asp Ser Ala Val
            100   105   110

Tyr Tyr Cys Ala Lys Ser Trp Ser Arg Asn Gly Asp Leu Asp Tyr Trp
            115   120   125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro
    130   135   140

Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr
145   150   155   160

Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr
            165   170   175

Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro
            180   185   190

Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr
    195   200   205

Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala
    210   215   220

His Pro Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu
225   230   235   240

Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro
            245   250   255

Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
            260   265   270

Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val
    275   280   285

24

```
Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp
    290                 295                 300

Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe
305                 310                 315                 320

Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp
                325                 330                 335

Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu
            340                 345                 350

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His
            355                 360                 365

Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys
    370                 375                 380

Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp
385                 390                 395                 400

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys
                405                 410                 415

Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr
            435                 440                 445

Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Glu Ser Leu Ser His Ser Pro Gly Lys
465                 470



<210> 21
<211> 1453
<212> DNA
<213> Canis familiaris

<400> 21
tcatttaccc ggagaatggg agagggattc ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
```

25

```
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg gagatggtcc tctcgatcgg 360
ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttccccttga gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcagggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgagggag tagagccctg aggactgcag 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
aggctcgggg aagtagcctg acaccaggca ggccagggcc accgtggagc cggaagtgga 960
cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
gaccagggtt ccctggcccc agtagtcaag atccccatta cgagaccagc tcttggcaca 1080
ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga gggtgttctt 1140
ggcgttgtct ctggagatgg tgaatcggcc cttcacagtc tgtgaatagg atgttcctgt 1200
gccatcaccg ttaatcccgg cgacccactg caggctcttg cctggagcct ggcggaccca 1260
gtccatggag tatcttctga aggtgaatcc agaggccaca caagagagtt tcagggaccc 1320
cccaggcttc accagggttc ctccagactc caccaaacgt acctcaccct ggacaccttt 1380
taaaatagtg acaaggaaaa cccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtcctgagc act                                                   1453


<210> 22
<211> 66
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(66)

<400> 22
ccc aaa aga gaa aat gga aga gtt cct cgc cca cct gat tgt ccc aaa    48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
 1               5                   10                  15

tgc cca gcc cct gaa atg                                            66
Cys Pro Ala Pro Glu Met
            20


<210> 23
<211> 22
<212> PRT
<213> Canis familiaris
```

<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
 1   5   10   15

Cys Pro Ala Pro Glu Met
                20

<210> 24
<211> 66
<212> DNA
<213> Canis familiaris

<400> 24
catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60
tttggg   66

<210> 25
<211> 938
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (37)..(753)

<220>
<223> At location 475, n = unknown

<400> 25
ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc   54
                                        Met Ser Ser Asp Met Ala
                                         1   5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg 102
Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp
            10   15   20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc 150
Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly
        25   30   35

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata 198
Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile
    40   45   50

27

```
ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc      246
Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val
 55                  60                  65                  70


ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt      294
Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe
                 75                  80                  85


tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc      342
Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu
                 90                  95                 100


cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg      390
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr
                105                 110                 115


ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt      438
Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly
                120                 125                 130


cag ccc aag gcc tcc ccc tcg gtc aca ctc ttc ccg ncc tyc tyt gag      486
Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu
135                 140                 145                 150


gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc      534
Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
                155                 160                 165


tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc      582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val
                170                 175                 180


acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag      630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
                185                 190                 195


tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct      678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser
                200                 205                 210


cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa      726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu
215                 220                 225                 230


aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg            773
Lys Lys Val Ala Pro Ala Lys Cys Ser
                235
```

cccaccaaag ggggctcaaa gcctcaggac ctccaggagg atcttgcctc ccatctgggt 833

catcccagcc attcccctta aacccaggca acattcaata aagtgttctt tcttcaatca 893

gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa   938

<210> 26
<211> 239
<212> PRT
<213> Canis familiaris
<223> At location 475, n = unknown

<400> 26
Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala
 1   5   10   15

His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser
                20   25   30

Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp
            35   40   45

Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro
        50   55   60

Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr
                85   90   95

Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                100   105   110

Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr
            115   120   125

Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu
            130   135   140

Phe Pro Xaa Xaa Xaa Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val
145   150   155   160

Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys
                165   170   175

Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser

29

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr
        195   200   205

Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His
    210   215   220

Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser
225   230   235

<210> 27
<211> 938
<212> DNA
<213> Canis familiaris

<220>
<223> At location 464, n = unknown

<400> 27
tttttttttt tttttttttt tttttttttt tttttttttt ttttctgatt gaagaaagaa 60
cactttattg aatgttgcct gggtttaagg ggaatggctg ggatgaccca gatgggaggc 120
aagatcctcc tggaggtcct gaggctttga gccccctttg gtgggcgggg ggcatcggga 180
acctaagagc actttgcggg ggccaccttt ttttccacgg ggctcccctc atgcgtgacc 240
aggcagctga agctgctgtg agatttccac ttgtcaggcg tcaggctcag gtagctgctg 300
gccgcgtact tgttgttgct ctgcttggag ggcttggtgg tctccacgcc ctgggtgacg 360
gggctgccgt ctgccttcca ggccaccgtc acgccgytgg ggtagaagtc gctgatgagg 420
cacaccaggg tggccttgtt ggcgccgagc tcctcaragr aggncgggaa gagtgtgacc 480
gagggggagg ccttgggctg accaaggaca gtcagttggg ttcctgagcc gaacacgtaa 540
acaccaagcg tggaatcaac agactgacag taataatcag cctcgtcctc agcctggagc 600
ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660
cctgagggtc gatccccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720
tggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780
accttctggc ccagggcccc agatactgag gccggctgat tcaacacagc ctgggcccag 840
gaccctgtgc agtgagcgag gagtgtgagg aggagagggg accaggccat gtcggaggac 900
atcactgatt gatcctgcct tctggggacc ctcgtgcc   938

<210> 28
<211> 578
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(423)

<220>
<223> At locations 471, 481, 522 and 549, n = unknown

<400> 28
```
cat caa gat tgg ttt aat ggt aag gag ttc aaa tgt aga gtc aac cac    48
His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
  1               5                  10                  15


ata gac ctc ccg tct ccc atc gag agg acc atc tct aag gcc aga ggg    96
Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
               20                  25                  30


agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca tcc cca aag gag   144
Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
           35                  40                  45


ttg tca tcc agt gac aca gtc agc atc acc tgc ctg ata aaa gac ttc   192
Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
       50                  55                  60


tac cca cct gac att gat gtg gag tgg cag agc aat gga cag cag gag   240
Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
 65                  70                  75                  80


cct gag agc aag tac cgc acg acc ccg ccc cag ctg gac gag gac ggg   288
Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
                85                  90                  95


tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc cgc tgg cag   336
Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
               100                 105                 110


cgg gga gac acc ttc ata tgt gcg gtg atg cat gaa gct cta cac aac   384
Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
           115                 120                 125


cac tac aca cag aaa tcc ctc tcc cat tct ccg ggt aaa tgagcaacac   433
His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
           130                 135                 140


gcccggcacc cagcaagccc cccacccttg gctctcanga tccctganga cacctgagcc 493

cctgtccctg tgtacataac cctgggtang cacccatcat gaaataaagc acccancact 553

gccctgggcc cttgcaaaaa aaaaa                                        578
```


31

<210> 29
<211> 141
<212> PRT
<213> Canis familiaris
<223> At locations 471, 481, 522 and 549, n = unknown

<400> 29
His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
 1   5   10   15

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
            20   25   30

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
        35   40   45

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
    50   55   60

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
65   70   75   80

Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
                85   90   95

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
            100   105   110

Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
        115   120   125

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
    130   135   140

<210> 30
<211> 578
<212> DNA
<213> Canis familiaris

<220>
<223> At locations 30, 57, 98 and 108, n = unknown

<400> 30
tttttttttt gcaagggccc agggcagtgn tgggtgcttt atttcatgat gggtgcntac 60
ccagggttat gtacacaggg acaggggctc aggtgtcntc agggatcntg agagccaagg 120
gtggggggct tgctgggtgc cgggcgtgtt gctcatttac ccggagaatg ggagagggat 180

32

ttctgtgtgt agtggttgtg tagagcttca tgcatcaccg cacatatgaa ggtgtctccc 240
cgctgccagc ggctcttgtc cacagagagc ttgctgtaca ggaagtagga cccgtcctcg 300
tccagctggg gcggggtcgt gcggtacttg ctctcaggct cctgctgtcc attgctctgc 360
cactccacat caatgtcagg tgggtagaag tcttttatca ggcaggtgat gctgactgtg 420
tcactggatg acaactcctt tggggatggc ggcaggacat acacactggg cttatgggcc 480
ctccctctgg ccttagagat ggtcctctcg atgggagacg ggaggtctat gtggttgact 540
ctacatttga actccttacc attaaaccaa tcttgatg 578

<210> 31
<211> 1364
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (59)..(1183)

<400> 31
ggcacgaggc cgattcacca tttccagaga caatgtcgag aacacgctgt atctgcag 58

atg aac agc ctg aga gct gag gat acg gcc ctg tat tac tgt aca agt 106
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
 1   5   10   15

ggg tta tgg atc aac tgg tac ggt ccg aat ttt gac tcc tgg ggc cag 154
Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
                20   25   30

gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt 202
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
            35   40   45

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 250
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
        50   55   60

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc 298
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
65   70   75   80

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc 346
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
                85   90   95

ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc 394
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
            100   105   110

33

```
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gcc cac ccg      442
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
        115                 120                 125

gcc agc aaa act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga      490
Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
        130                 135                 140

aga gtt cct cgc cca cct gat tgt ccc aaa tgc cca acc cct gaa atg      538
Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145                 150                 155                 160

ctg gga ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc      586
Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
                165                 170                 175

ctc ttg att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg      634
Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
                180                 185                 190

gac cca gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag      682
Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
                195                 200                 205

cag atg caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc      730
Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly
        210                 215                 220

acc tac cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc      778
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu
225                 230                 235                 240

aag ggg aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc      826
Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser
                245                 250                 255

cca atc gag agg acc atc tcc aag gcc aga ggg cag gcc cat caa ccc      874
Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro
                260                 265                 270

agt gtg tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca      922
Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr
                275                 280                 285

gtc agc ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat      970
Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp
        290                 295                 300
```

34

```
gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc    1018
Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
305                 310                 315                 320

acg acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc    1066
Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
                325                 330                 335

aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata    1114
Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
            340                 345                 350

tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc    1162
Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
            355                 360                 365

ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc       1213
Leu Ser His Ser Pro Gly Lys
        370                 375

cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa  1273

ccccgggtag gcacctggca tgaaataaag cacccagtac tgccctggaa aaaaaaaaaa  1333

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                                 1364


<210> 32
<211> 375
<212> PRT
<213> Canis familiaris

<400> 32
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
  1               5                  10                  15

Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
                20                  25                  30

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
            35                  40                  45

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
        50                  55                  60

Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
  65                  70                  75                  80
```

35

Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
                85   90   95

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
            100   105   110

Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
            115   120   125

Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
        130   135   140

Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145   150   155   160

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
                165   170   175

Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
            180   185   190

Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
            195   200   205

Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly
        210   215   220

Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu
225   230   235   240

Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser
                245   250   255

Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro
            260   265   270

Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr
            275   280   285

Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp
        290   295   300

Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
305   310   315   320

Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
            325   330   335

36

Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
          340   345   350

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
          355   360   365

Leu Ser His Ser Pro Gly Lys
    370   375

<210> 33
<211> 1364
<212> DNA
<213> Canis familiaris

<400> 33
tttttttttt tttttttttt tttttttttt tttttttttt tttccagggc agtactgggt 60
gctttatttc atgccaggtg cctacccggg gttatgtaca cagggatggg ggctcaggca 120
tcctcatggg atcctgaaag ccaagggtgg ggggcttgct gggtgccggg cgtgttgctc 180
atttacccgg agaatgggag agggatttct gtgtgtagtg gttgtgtaaa gcttcatgca 240
tcaccgcaca tatgaaggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300
tgtacaggaa gtaggacccg tcctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360
caggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg aagaagtctt 420
tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctcccgggat ggcggcagga 480
catacacact gggttgatgg gcctgccctc tggccttgga gatggtcctc tcgattgggg 540
atgggagggc tttgttgttg actttgcacg tgaactgctt ccccttgagc cagtcctggt 600
gcccaatggg gaggacactg accacacggt aggtgccatt gaactgctcc tcacgaggct 660
gagtcttggc tgtttgcatc tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720
cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780
tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcaggggttg 840
ggcatttggg acaatcaggt gggcgaggaa ctcttccatt ttctcttttg ggcactggct 900
tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaaggtc tcgctgggcc 960
acctgctgga gggcactgtc accatgctgc tgagggagta gagccctgag gactgcagga 1020
cggacgggaa ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag 1080
gctcggggaa gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc 1140
cgcagctggg ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gagacggtga 1200
ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataacccac 1260
ttgtacagta atacagggcc gtatcctcag ctctcaggct gttcatctgc agatacagcg 1320
tgttctcgac attgtctctg gaaatggtga atcggcctcg tgcc   1364

<210> 34
<211> 1168
<212> DNA
<213> Canis familiaris

37

<220>
<221> CDS
<222> (48)..(1166)

<400> 34
ccaggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct   56
                                                        Met Glu Ser
                                                         1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt   104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
      5   10   15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg   152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 20   25   30   35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat   200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                 40   45   50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc   248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
                 55   60   65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag   296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
             70   75   80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc   344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
     85   90   95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg   392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
100   105   110   115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat   440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                 120   125   130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt   488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
                 135   140   145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc   536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
         150   155   160

38

```
ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc      584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
    165                 170                 175

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc      632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
180                 185                 190                 195

ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc      680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro
            200                 205                 210

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg      728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro
            215                 220                 225

gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc      776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys
        230                 235                 240

aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg      824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser
        245                 250                 255

gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga      872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg
260                 265                 270                 275

aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct      920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro
            280                 285                 290

gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc      968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala
            295                 300                 305

aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc     1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val
            310                 315                 320

agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc     1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe
            325                 330                 335

aag tgc aga gtc aac cac ata ggc ccc ccg tcc ccc atc gag agg act     1112
Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile Glu Arg Thr
340                 345                 350                 355
```

39

```
atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg      1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu
            360                 365                 370

ccg cca tc                                                           1168
Pro Pro


<210> 35
<211> 373
<212> PRT
<213> Canis familiaris

<400> 35
Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly
  1               5                  10                  15

Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
            35                  40                  45

Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
      50                  55                  60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
 65                  70                  75                  80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
                  85                  90                  95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
            100                 105                 110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
            115                 120                 125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
            130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
145                 150                 155                 160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
                  165                 170                 175
```

40

```
Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
            195                 200                 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
            210                 215                 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225                 230                 235                 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
            260                 265                 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
            275                 280                 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
            290                 295                 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
                325                 330                 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile
            340                 345                 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
            355                 360                 365

Tyr Val Leu Pro Pro
    370
```

<210> 36
<211> 1168
<212> DNA
<213> Canis familiaris

<400> 36
gatggcggca ggacatacac actgggctga tgggcttgcc ctctggcttt ggagatagtc 60

41

```
ctctcgatgg gggacggggg gcctatgtgg ttgactctgc acttgaactc ctttccggtg 120
agccagtcct ggtgctcaat ggggaggacg ctgaccacac ggtaggtgct gttgaactgc 180
tgctcacgag gctgcgtctt ggctgtgtgc acctccttac catccacgaa ccagctgatc 240
tgcacctcag ggtcctcacg gcccagatct aacaccacac aggtgatctc gggtgttcgg 300
gtaatcctga ggatgtcctt gggtttcggg ggaaagatga agaccgaagg ccctcccagt 360
gattcaggga ctgggcatgg ggatatacac ttgcaggtgg actctttggg cactggcttg 420
tctactttag tgttgctggc cgggtggacc acgttgcagg tgaaggtctc gctgggccac 480
ctgctggagg gcactgtcac cgtgctgctg agggagtaga gccctgagga ctgcaggacg 540
gacgggaagg tgtgcacacc gctggtcaag gagccggaat tccaggacac agttacaggc 600
tcggggaagt agcctgacac caggcaggcc agggccaccg tggagccgga agtggacccg 660
cagctggggg ccagtgggaa aaccgagggg gccgtggtgg aggctgagga cacgaagagt 720
gaggtgccat tgccccagtg gtccatacca taataatgtc gcggccatac tcccgtcaca 780
cagtgataga ttgccgtgtc ctcggctttc aggctgctca tctggagata cagcgtgttc 840
ttggcgttgt ctctggagat ggtgaatcgg cccttcacag cgtctgcgta gtaagtatct 900
ccacgattgc taacagctgc gacccactgc agccccttcc ctggagactg acggacccaa 960
ctcatgccat agtcactgaa ggtgaatcca gaggccacac aggacagtct caaggacccc 1020
ccaggcttca ccaggtctcc cccagactcc accagttgca cctcaccctg gacacctttt 1080
aaaatagaga caaggaaaac ccagcagagc acagactcca tggtggtttg tctgtgttgt 1140
gtcctgagca ctgaatgggg tcacctgg                                     1168
```

<210> 37
<211> 1059
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1056)

<400> 37
```
tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat ggc acc tca   48
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
 1               5                   10                  15


ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg   96
Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
            20                  25                  30


gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc   144
Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
        35                  40                  45


ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc   192
Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
    50                  55                  60


gac tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc   240
```
```
                                        42
```

```
Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
 65                  70                  75                  80


tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc tcc agc agg     288
Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
                 85                  90                  95


tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg gcc agc aac     336
Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
                100                 105                 110


act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt ata     384
Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
            115                 120                 125


tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc atc     432
Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
        130                 135                 140


ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc gag     480
Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145                 150                 155                 160


atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg cag     528
Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
                165                 170                 175


atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg cag     576
Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
                180                 185                 190


cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc ctc     624
Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            195                 200                 205


ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc aga     672
Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
        210                 215                 220


gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc aaa     720
Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225                 230                 235                 240


gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca tcc     768
Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
                245                 250                 255


cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg atc     816
```

43

```
Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
        260                 265                 270

aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag agc aat gga    864
Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
        275                 280                 285

cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg gac    912
Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
        290                 295                 300

gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc    960
Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305                 310                 315                 320

cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa gct   1008
Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
                325                 330                 335

cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt aaa   1056
Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
                340                 345                 350

tga                                                                1059


<210> 38
<211> 352
<212> PRT
<213> Canis familiaris

<400> 38
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
  1               5                  10                  15

Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
                20                  25                  30

Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
            35                  40                  45

Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
        50                  55                  60

Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
65                  70                  75                  80

Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
```

44

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
            100   105   110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
            115   120   125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
            130   135   140

Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
145   150   155   160

Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
                165   170   175

Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
            180   185   190

Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            195   200   205

Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
            210   215   220

Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225   230   235   240

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
                245   250   255

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
            260   265   270

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
            275   280   285

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
290   295   300

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305   310   315   320

Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
                325   330   335

Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys

45

<210> 39
<211> 1059
<212> DNA
<213> Canis familiaris

<400> 39
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagcttcatg 60
catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatggtgg 300
caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc 420
ctggtgctca atggggagga cgctgaccac acggtaggtg ctgttgaact gctgctcacg 480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
aggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660
gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt 720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780
gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840
ggtgtgcaca ccgctggtca aggagtcgga attccaggac acagttacag gctcggggaa 900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960
ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020
attgccccag tggtccatac cataataatg tcgcggcca   1059

<210> 40
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 15 and 21, n = unknown

<400> 40
caycargayt ggytnaaygg naargartty aartgy   36

<210> 41
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 41
gccctccagc aggtggccca gcgagacc   28

<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 42
ggggatggcg gcaggacata cac   23

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 43
tttacccgga gaatgggaga ggg   23

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 44
ggtctgcgtg ggccacctgc tggagggc   28

<210> 45
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 45
gggtggggggg cttgctgggt gccgggcg   28

<210> 46
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 46
ccaggtgacc ccattcagtg ctcaggacac   30

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 47
ctgtgtgacg ggagtatggc cgcgac   26

<210> 48
<211> 483
<212> DNA
<213> Canis familiaris

<220>
<223> At location 470, n = unknown

48

<400> 48

cttatttgga catggaaccc cccagagggc gccagcccga attgcacctt acggtatttt 60

agtcattttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120

gtacccctga atgagaggat ttgtctgcaa gtggggtccc agtgcagcac caatgaaagt 180

gacaatccta gcattttggt ggaaaagtgc accccaccac ctgaaggtgg tcctgagtcg 240

gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300

cctggaagga atacaagccc tgacaccaac tatactctct actattggca gcagcctg 360

ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420

gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatggtcaag 480

gtt 483

<210> 49
<211> 1547
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1215)

<400> 49

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ggc ggg gtc gcc gca ccc acc gaa act cag cca cct gtg acg aat ttg    48
Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
 1               5                  10                  15

agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct    96
Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
            20                  25                  30

ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt   144
Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
        35                  40                  45

gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa   192
Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
    50                  55                  60

gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc   240
Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
65                  70                  75                  80

agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc   288
Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
                85                  90                  95

cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt   336
```

```
Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys
            100             105             110

gtt tgg cac aac ctg agc tac atg aag tgt act tgg ctt cct gga agg    384
Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg
        115             120             125

aat aca agc cct gac acc aac tat act ctc tac tat tgg cac agc agc    432
Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser
    130             135             140

ctg gga aaa att ctt caa tgc gaa gac atc tat aga gaa ggt caa cac    480
Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His
145             150             155             160

att ggt tgt tcc ttt gct ctg act aat ttg aag gat tcc agt ttt gaa    528
Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu
                165             170             175

caa cac agt gtc caa ata atg gtc aag gat aat gca aga aaa att aga    576
Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg
            180             185             190

ccg tcc ttc aat ata gtg cct tta act tct cat gtg aaa cct gat ccc    624
Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro
        195             200             205

ccc cat att aag cgt ctc ttc ttc caa aat ggt aac ttg tat gtg caa    672
Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln
    210             215             220

tgg aag aat cca caa aat ttt tat agc aga tgc tta tct tac caa gta    720
Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val
225             230             235             240

gaa gtc aat aac agc cag act gag acg aat gat ata ttc tac gtt gaa    768
Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu
            245             250             255

gaa gcc aaa tgt cag aat tca gaa ttt gag gga aac ctg gag ggt aca    816
Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr
            260             265             270

att tgt ttc atg gtc ccc ggc gtt ctt cct gat act ttg aac aca gtc    864
Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val
        275             280             285

aga ata aga gtc aga aca aat aag tta tgc tat gag gat gac aaa ctc    912
```

50

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
    290   295   300

tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc   960
Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
305   310   315   320

acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt   1008
Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
                325   330   335

gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata   1056
Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
                340   345   350

ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga   1104
Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
                355   360   365

gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag   1152
Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
    370   375   380

aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg   1200
Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
385   390   395   400

aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt   1255
Lys Lys Ala Ser Gln
                405

aaagattcat ccccacgttc tcgggaagct tcaaggtcaa gcatcttggg aaaggacatt 1315

acagtttcta cagcatggtg tacctgggca tctccgacta cttcttcaac acagcagggc 1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

aatccaaatt ccgactgaca accgattttt tggggaccct cataccccaa gtggccgaga 1495

tgttccccaa catgacggtt caattcaacg tctgggcctc ctccccgccg ca   1547

<210> 50
<211> 405
<212> PRT
<213> Canis familiaris

<400> 50

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Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
 1               5                   10                  15

Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
                20                  25                  30

Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
            35                  40                  45

Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
        50                  55                  60

Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
65              70                  75                      80

Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
                85                  90                  95

Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys
            100                 105                 110

Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg
        115                 120                 125

Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser
    130                 135                 140

Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His
145                 150                 155                 160

Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu
            165                 170                 175

Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg
            180                 185                 190

Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro
        195                 200                 205

Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln
    210                 215                 220

Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val
225                 230                 235                 240

Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu
            245                 250                 255
```

52

Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr
            260   265   270

Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val
            275   280   285

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu
            290   295   300

Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro
305   310   315   320

Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly
            325   330   335

Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile
            340   345   350

Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly
            355   360   365

Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu
            370   375   380

Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu
385   390   395   400

Lys Lys Ala Ser Gln
                405

<210> 51
<211> 1547
<212> DNA
<213> Canis familiaris

<400> 51
tgcggcgggg aggaggccca gacgttgaat tgaaccgtca tgttggggaa catctcggcc   60
acttggggta tgagggtccc caaaaaatcg gttgtcagtc ggaatttgga tttctttggt   120
atcatgtcgt ccgtgatggt catgtttaag gcccctgcct cttggtacac aagccctgct   180
gtgttgaaga agtagtcgga gatgcccagg tacaccatgc tgtagaaact gtaatgtcct   240
ttcccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggtc   300
atgctgaagg ctaaaataag ttatccccat tactgagagg ctttcttcag gttttcaatc   360
agcactactg agtccgtttc ttcttttgtt tgcttctcat agatgtcgta cttcctccag   420
tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga   480
attggaggga atataatgat cttgagcctt ttgagataaa gcagaaggat tatgatggca   540
cctgcaacga tgacttgagt ggcgagcaac atggttatat agaacgtggg gtcggtattc   600

                              53

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tcacctatac tcatcgcttg actccaatta ctccagagtt tgtcatcctc atagcataac 660
ttatttgttc tgactcttat tctgactgtg ttcaaagtat caggaagaac gccgggggacc 720
atgaaacaaa ttgtaccctc caggtttccc tcaaattctg aattctgaca tttggcttct 780
tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
aagcatctgc tataaaaatt ttgtggattc ttccattgca catacaagtt accattttgg 900
aagaagagac gcttaatatg ggggggatca ggtttcacat gagaagttaa aggcactata 960
ttgaaggacg gtctaatttt tcttgcatta tccttgacca ttatttggac actgtgttgt 1020
tcaaaactgg aatccttcaa attagtcaga gcaaaggaac aaccaatgtg ttgaccttct 1080
ctatagatgt cttcgcattg aagaattttt cccaggctgc tgtgccaata gtagagagta 1140
tagttggtgt cagggcttgt attccttcca ggaagccaag tacacttcat gtagctcagg 1200
ttgtgccaaa cacattgtag ctcagtcaca gccgactcag gatcaccttc aggtggtggg 1260
gtgcacttt ccaccaaaat gctaggattg tcactttcat tggtgctgca ctgggacccc 1320
acttgcagac aaatcctctc attcaggggt acttcttttg aacgatgagt ttcaggagca 1380
atttcttat cctgtttgtt gtcaaaatga ctaaaatacc gtaaggtgca attcgggctg 1440
gctccctcgg gagggttcca tgtccatatg accgtgcaga ggttttcaac agaaacactc 1500
aaattcgtca caggtggctg agtttcggtg ggtgcggcga ccccgcc 1547
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<210> 52
<211> 1215
<212> DNA
<213> Canis familiaris

<400> 52
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ggcggggtcg ccgcacccac cgaaactcag ccacctgtga cgaatttgag tgtttctgtt 60
gaaaacctct gcacggtcat atggacatgg aaccctcccg agggagccag cccgaattgc 120
accttacggt attttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgtc tgcaagtggg gtcccagtgc 240
agcaccaatg aaagtgacaa tcctagcatt ttggtggaaa agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttcctgg aaggaataca agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcgaagaca tctatagaga aggtcaacac 480
attggttgtt cctttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt ccttcaatat agtgccttta 600
acttctcatg tgaaacctga tcccccccat attaagcgtc tcttcttcca aaatggtaac 660
ttgtatgtgc aatggaagaa tccacaaaat ttttatagca gatgcttatc ttaccaagta 720
gaagtcaata acagccagac tgagacgaat gatatattct acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggt ccccggcgtt 840
cttcctgata cttttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
acgttctata taaccatgtt gctcgccact caagtcatcg ttgcaggtgc catcataatc 1020
cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagattttta aagaaatgtt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
gacatctatg agaagcaaac aaaagaagaa acggactcag tagtgctgat tgaaaacctg 1200
aagaaagcct ctcag 1215
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<210> 53
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<211> 1215
<212> DNA
<213> Canis familiaris

<400> 53
ctgagaggct ttcttcaggt tttcaatcag cactactgag tccgtttctt cttttgtttg 60
cttctcatag atgtcgtact tcctccagtg cagcgtatca tcattctggt ctccaaacat 120
ttctttaaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt 180
gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240
ggttatatag aacgtggggt cggtattctc acctatactc atcgcttgac tccaattact 300
ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360
caaagtatca ggaagaacgc cggggaccat gaaacaaatt gtaccctcca ggtttccctc 420
aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtctg 480
gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540
ccattgcaca tacaagttac cattttggaa gaagagacgc ttaatatggg ggggatcagg 600
tttcacatga gaagttaaag gcactatatt gaaggacggt ctaattttc ttgcattatc 660
cttgaccatt atttggacac tgtgttgttc aaaactggaa tccttcaaat tagtcagagc 720
aaaggaacaa ccaatgtgtt gaccttctct atagatgtct cgcattgaa gaattttcc 780
caggctgctg tgccaatagt agagagtata gttggtgtca gggcttgtat ccttccagg 840
aagccaagta cacttcatgt agctcaggtt gtgccaaaca cattgtagct cagtcacagc 900
cgactcagga tcaccttcag gtggtggggt gcacttttcc accaaaatgc taggattgtc 960
actttcattg gtgctgcact gggaccccac ttgcagacaa atcctctcat tcaggggtac 1020
ttcttttgaa cgatgagttt caggagcaat tttcttatcc tgtttgttgt caaaatgact 1080
aaaataccgt aaggtgcaat tcgggctggc tccctcggga gggttccatg tccatatgac 1140
cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcggtggg 1200
tgcggcgacc ccgcc 1215


<210> 54
<211> 620
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (184)..(618)

<400> 54
ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60

aattaatgtc tccaaactgg agaagagaaa aaaagagga cctgtgataa ttgcctatga 120

taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180

gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt    228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
      1               5                  10                  15

55

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt    276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
                    20                  25                  30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat    324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
                    35                  40                  45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa    372
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
                50                  55                  60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac    420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
        65                  70                  75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat    468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
80                  85                  90                  95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa    516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
                    100                 105                 110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat    564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
                    115                 120                 125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac    612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
                130                 135                 140

tgt gta ta                                                          620
Cys Val
        145


<210> 55
<211> 145
<212> PRT
<213> Canis familiaris

<400> 55
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
1               5                   10                  15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
                    20                  25                  30

56

```
Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
        35                  40                  45


Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
    50                  55                  60


Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65                  70                  75                  80


Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
                85                  90                  95


Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
            100                 105                 110


Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
            115                 120                 125


Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
    130                 135                 140


Val
145




<210> 56
<211> 620
<212> DNA
<213> Canis familiaris

<400> 56
tatacacagt ccatatcttg aattttagtt tcccgatttc cttgtggtga tgtccaataa 60
gtagtttctg cccatgaact tctaacttct gatccatttg tgcattgtgc tggcagaagt 120
gtgtttatct ttgcttcaat acctttgtta agatcaaacc catctttgta atgtagattc 180
ttggtaatga tggtcttcca gttttcacta tcaatgtttc ggtattttaa ttcatattct 240
attgtgcatt ccttaaaatt atccggaaat aatggaggtt gccattgcaa agagagataa 300
cctaaatatc cagggtccac tatctcaaaa tcctgaggag gattaacttt tatctcagca 360
tttgaaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420
aaatgaatga aagccattcc tccaagattc aatactttga gtttccact caataatatg 480
gtttctcaag aaatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540
ccagtttgga gacattaatt agaatctcta agacttccct tcctgtctga taatcaagca 600
cacaaactca gcctcgtgcc                                              620


<210> 57
<211> 878
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<400> 57
caa gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac   48
Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr
 1   5   10   15

aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat   96
Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His
             20   25   30

ttt gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat   144
Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
         35   40   45

tca gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga   192
Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
     50   55   60

tgc agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc   240
Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
 65   70   75   80

tgt gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt   288
Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
                 85   90   95

att ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt   336
Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
                100   105   110

agt ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg   384
Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
             115   120   125

cct aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc   432
Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
         130   135   140

aca gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata   480

58

```
Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
145                 150             155                 160


caa atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta    528
Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
                165             170                 175


aga agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag    576
Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
            180             185                 190


tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta    624
Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
        195             200                 205


gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta    672
Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
    210             215                 220


ata act tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc    720
Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
225             230                 235                 240


ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt        765
Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
                245             250                 255


tgactcagta actttcagtc ttatggccag atgttaaata tgagtcttat taaactgaag  825


cttttcctca aatattgaat aaatcttatt ttaaaangaa aaaaaaaaaa aaa         878



<210> 58
<211> 255
<212> PRT
<213> Canis familiaris
<223> At location 862, n = unknown

<400> 58
Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr
 1               5                   10                  15


Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His
            20                  25                  30


Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
        35                  40                  45
```

59

Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
    50   55   60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
    65   70   75   80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
                   85   90   95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
             100   105   110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
          115   120   125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
          130   135   140

Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
145   150   155   160

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
             165   170   175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
          180   185   190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
          195   200   205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
          210   215   220

Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
225   230   235   240

Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
          245   250   255

<210> 59
<211> 878
<212> DNA
<213> Canis familiaris

<400> 59
tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60

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ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgtttttcag taaagcccctt 180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
atcaagaaaa atactaaggt ttccttccat atgtcaccttt tccagcattg ttcatcactc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggtctgatag ctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtccatat cttgaatttt agtttcccga tttccttg 878


<210> 60
<211> 1454
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (184)..(1341)

<220>
<223> At location 1438, n = unknown

<400> 60
ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60

aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120

taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180

gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt    228
    Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
    1               5                   10                  15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt    276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
                20                  25                  30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat    324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
            35                  40                  45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa    372
```

61

Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
        50   55   60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac   420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
        65   70   75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat   468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 80   85   90   95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa   516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
                100   105   110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat   564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
                115   120   125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac   612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
                130   135   140

tgt gta tat tac aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc   660
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly
        145   150   155

atg ggt gtc cat ttt gat acc aat tac cag ttg ttt tac tgg tat gag   708
Met Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu
160   165   170   175

ggc ttg gac cat tca gca gag tgt act gat tac atc aag gtt aat gga   756
Gly Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly
                180   185   190

aaa aat atg gga tgc agg ttt ccc tat ttg gag tca tca gac tat aaa   804
Lys Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys
                195   200   205

gat ttc tac atc tgt gtt aat ggg tca tca gaa tcc cag cct atc aga   852
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg
                210   215   220

ccc agc tat ttt att ttt cag ctt caa aat ata gtt aaa cct atg cca   900
Pro Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro
        225   230   235

cca gac tac ctt agt ctt act gtg aag aat tca gag gaa att aac ctg   948

62

```
Pro Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu
240                 245             250             255


aaa tgg aac atg cct aaa gga ccc att cca gcc aaa tgt ttc att tat     996
Lys Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr
                260             265             270


gaa att gaa ttc aca gag gat ggt act act tgg gtg act acc aca gtt    1044
Glu Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val
                275             280             285


gag aat gag ata caa atc aca aga aca tca aat gaa agc caa aaa tta    1092
Glu Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu
            290             295             300


tgc ttt ttg gta aga agt aaa gtg aat att tat tgc tca gat gat gga   1140
Cys Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
    305             310             315


atc tgg agt gag tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg   1188
Ile Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp
320             325             330             335


aag gaa acc tta gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata  1236
Lys Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile
                340             345             350


ttt gtt ttg gta ata act tgc ctg ctt ttg tat aag caa agg gct tta  1284
Phe Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu
                355             360             365


ctg aaa acg atc ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac  1332
Leu Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp
            370             375             380


aca ttc tgt tgactcagta actttcagtc ttatggccag atgttaaata          1381
Thr Phe Cys
        385


tgagtcttat taaactgaag cttttcctca atatttgaat aaatcttatt ttaaaangaa 1441


aaaaaaaaaa aaa                                                    1454



<210> 61
<211> 386
<212> PRT
<213> Canis familiaris
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<223> At location 1438, n = unknown

<400> 61
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val
1   5   10   15

Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
                20   25   30

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
                35   40   45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
            50   55   60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
65   70   75   80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
                    85   90   95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
                100   105   110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
            115   120   125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
        130   135   140

Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met
145   150   155   160

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly
            165   170   175

Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys
            180   185   190

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp
        195   200   205

Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro
    210   215   220

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro
225   230   235   240

64

Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys
                245   250   255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu
                260   265   270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu
                275   280   285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys
        290   295   300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile
305   310   315   320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys
                325   330   335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe
                340   345   350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu
        355   360   365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr
        370   375   380

Phe Cys
385

<210> 62
<211> 1454
<212> DNA
<213> Canis familiaris

<220>
<223> At location 17, n = unknown

<400> 62
ttttttttt ttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60
ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
atcaagaaaa atactaaggt ttccttccat atgtcacctt ccagcattg ttcatcactc 300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420

65

```
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
cagtccatat cttgaatttt agtttcccga tttccttgtg gtgatgtcca ataagtagtt 900
tctgcccatg aacttctaac ttctgatcca tttgtgcatt gtgctggcag aagtgtgttt 960
atctttgctt caataccttt gttaagatca aacccatctt tgtaatgtag attcttggta 1020
atgatggtct tccagttttc actatcaatg tttcggtatt ttaattcata ttctattgtg 1080
cattccttaa aattatccgg aaataatgga ggttgccatt gcaaagagag ataacctaaa 1140
tatccagggt ccactatctc aaaatcctga ggaggattaa cttttatctc agcatttgaa 1200
agcatagagc caaatgctgt gcaaacaagc agggtataga ggaatccgac atccaaatga 1260
atgaaagcca ttcctccaag attcaatact ttgaagtttc cactcaataa tatggtttct 1320
caagaaatga attatcatag gcaattatca caggtcctct tttttttctc ttctccagtt 1380
tggagacatt aattagaatc tctaagactt cccttcctgt ctgataatca agcacacaaa 1440
ctcagcctcg tgcc                                                  1454


<210> 63
<211> 1158
<212> DNA
<213> Canis familiaris

<400> 63
atggctttca ttcatttgga tgtcggattc ctctataccc tgcttgtttg cacagcattt 60
ggctctatgc tttcaaatgc tgagataaaa gttaatcctc ctcaggattt tgagatagtg 120
gaccctggat atttaggtta tctctctttg caatggcaac ctccattatt ccggataat 180
tttaaggaat gcacaataga atatgaatta aaataccgaa acattgatag tgaaaactgg 240
aagaccatca ttaccaagaa tctacattac aaagatgggt ttgatcttaa caaaggtatt 300
gaagcaaaga taaacacact tctgccagca caatgcacaa atggatcaga agttagaagt 360
tcatgggcag aaactactta ttggacatca ccacaaggaa atcgggaaac taaaattcaa 420
gatatggact gtgtatatta caactggcaa tatttagtct gctcttggaa acctggcatg 480
ggtgtccatt ttgataccaa ttaccagttg ttttactggt atgagggctt ggaccattca 540
gcagagtgta ctgattacat caaggttaat ggaaaaaata tgggatgcag gtttccctat 600
ttggagtcat cagactataa agatttctac atctgtgtta atgggtcatc agaatcccag 660
cctatcagac ccagctattt tattttttcag cttcaaaata tagttaaacc tatgccacca 720
gactacctta gtcttactgt gaagaattca gaggaaatta acctgaaatg gaacatgcct 780
aaaggaccca ttccagccaa atgtttcatt tatgaaattg aattcacaga ggatggtact 840
acttgggtga ctaccacagt tgagaatgag atacaaatca caagaacatc aaatgaaagc 900
caaaaattat gcttttggt aagaagtaaa gtgaatattt attgctcaga tgatggaatc 960
tggagtgagt ggagtgatga acaatgctgg aaaggtgaca tatggaagga aaccttagta 1020
tttttcttga taccatttgc ttttgtctca atatttgttt tggtaataac ttgcctgctt 1080
ttgtataagc aaagggcttt actgaaaacg atctttcata caaaaaaaga agtctttttct 1140
catcaagaca cattctgt                                             1158
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66

<210> 64
<211> 1158
<212> DNA
<213> Canis familiaris

<400> 64
acagaatgtg tcttgatgag aaaagacttc ttttttttgta tgaaagatcg ttttcagtaa 60
agcccttttgc ttatacaaaa gcaggcaagt tattaccaaa acaaatattg agacaaaagc 120
aaatggtatc aagaaaaata ctaaggtttc cttccatatg tcacctttcc agcattgttc 180
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aatttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 540
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 660
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 720
atatacacag tccatatctt gaatttttagt ttcccgattt ccttgtggtg atgtccaata 780
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 900
cttggtaatg atggtcttcc agttttcact atcaatgttt cggtatttta attcatattc 960
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc atagagccaa atgctgtgca acaagcagg gtatagagga atccgacatc 1140
caaatgaatg aaagccat 1158

<210> 65
<211> 1095
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1095)

<400> 65
tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat ttt   48
Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
 1   5   10   15

gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa   96
Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
            20   25   30

cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa   144
Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

```
tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att acc    192
Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
     50                    55                    60


aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att gaa    240
Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
 65                    70                    75                    80


gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca gaa    288
Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
                 85                    90                    95


gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa gga    336
Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
             100                   105                   110


aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac tgg    384
Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
         115                   120                   125


caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt gat    432
Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
     130                   135                   140


acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca gca    480
Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145                   150                   155                   160


gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc agg    528
Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
                 165                   170                   175


ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt gtt    576
Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
             180                   185                   190


aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att ttt    624
Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
         195                   200                   205


cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt ctt    672
Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
     210                   215                   220


act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa    720
Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys
```

```
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag    768
Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
            245                 250                 255

gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc    816
Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
            260                 265                 270

aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt    864
Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
            275                 280                 285

aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt    912
Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser
            290                 295                 300

gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt    960
Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
305                 310                 315                 320

ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act    1008
Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
            325                 330                 335

tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat    1056
Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
            340                 345                 350

aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt                1095
Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
            355                 360                 365
```

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<210> 66
<211> 365
<212> PRT
<213> Canis familiaris

<400> 66
Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
  1               5                  10                  15

Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
            20                  25                  30

Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu
```

69

35   40   45

Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
    50   55   60

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
65   70   75   80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
                85   90   95

Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
            100   105   110

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
            115   120   125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
    130   135   140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145   150   155   160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
                165   170   175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
            180   185   190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
            195   200   205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
    210   215   220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys
225   230   235   240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
                245   250   255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
            260   265   270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
            275   280   285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser

                                70

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
305   310   315   320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
                    325   330   335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
                    340   345   350

Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
            355   360   365

<210> 67
<211> 1095
<212> DNA
<213> Canis familiaris

<400> 67
acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60
agccctttgc ttatacaaaa gcaggcaagt tattaccaaa acaaatattg agacaaaagc 120
aaatggtatc aagaaaaata ctaaggtttc cttccatatg tcacctttcc agcattgttc 180
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aattttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 540
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 660
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 720
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 780
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 900
cttggtaatg atggtcttcc agttttcact atcaatgttt cggtatttta attcatattc 960
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc ataga 1095

<210> 68
<211> 954
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(954)

<400> 68
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat   48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
1   5   10   15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg   96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
           20   25   30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat   144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
           35   40   45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att   192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
      50   55   60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att   240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65   70   75   80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca   288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
              85   90   95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa   336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
           100   105   110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac   384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
           115   120   125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt   432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca   480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc   528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
           165   170   175

72

```
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt    576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180                 185                 190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att    624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195                 200                 205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt    672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210                 215                 220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct    720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca    768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa    816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260                 265                 270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga    864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275                 280                 285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg    912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290                 295                 300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc            954
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
305                 310                 315


<210> 69
<211> 318
<212> PRT
<213> Canis familiaris

<400> 69
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                   10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
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73

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35   40   45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
            165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180   185   190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
            245   250   255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
            260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg

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            275                    280                    285
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290                    295                    300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
305                    310                    315




<210> 70
<211> 954
<212> DNA
<213> Canis familiaris

<400> 70
ggtttccttc cagatatcac ctttccagca ttgttcatca ctccactcac tccagattcc 60
atcatctgag caataaatat tcactttact tcttaccaaa aagcataatt tttggctttc 120
atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180
atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcat 240
gttccatttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctggtgg 300
cataggttta actatatttt gaagctgaaa aataaaatag ctgggtctga taggctggga 360
ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataggg 420
aaacctgcat cccatatttt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480
gtccaagccc tcataccagt aaaacaactg gtaattggta tcaaaatgga cacccatgcc 540
aggtttccaa gagcagacta atattgcca gttgtaatat acacagtcca tatcttgaat 600
tttagtttcc cgatttcctt gtggtgatgt ccaataagta gtttctgccc atgaacttct 660
aacttctgat ccatttgtgc attgtgctgg cagaagtgtg tttatctttg cttcaatacc 720
tttgttaaga tcaaacccat ctttgtaatg tagattcttg gtaatgatgg tcttccagtt 780
ttcactatca atgtttcggt attttaattc atattctatt gtgcattcct taaaattatc 840
cggaaataat ggaggttgcc attgcaaaga gagataacct aaatatccag ggtccactat 900
ctcaaaatcc tgaggaggat taactttat ctcagcattt gaaagcatag acat      954




<210> 71
<211> 1686
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1683)

<400> 71
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat   48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1               5                  10                  15
```

```
ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg      96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                20                  25                  30


caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat     144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
                35                  40                  45


gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att     192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
        50                  55                  60


acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att     240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80


gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca     288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                    85                  90                  95


gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa     336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
                100                 105                 110


gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac     384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
                115                 120                 125


tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt     432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140


gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca     480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160


gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc     528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165                 170                 175


agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt     576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
                180                 185                 190


gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att     624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
                195                 200                 205
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76

```
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt      672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210                 215                 220


ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct      720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240


aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca      768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255


gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa      816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
                260                 265                 270


atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga      864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
                275                 280                 285


agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg      912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290                 295                 300


agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc      960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320


aac act aaa gta gac aag cca gtg ttc aat gaa tgc aga tgc act gat     1008
Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
                325                 330                 335


aca ccc cca tgc cca gtc cct gaa cct ctg gga ggg cct tcg gtc ctc     1056
Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
                340                 345                 350


atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc     1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
                355                 360                 365


gag gtc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg     1152
Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
    370                 375                 380


cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acc     1200
Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385                 390                 395                 400
```

77

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cag tct cgt gag cag cag ttc aac ggc acc tac cgt gtg gtc agc gtc      1248
Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
                405                 410                 415

ctc ccc att gag cac cag gac tgg ctc aca ggg aag gag ttc aag tgc      1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                420                 425                 430

aga gtc aac cac ata gac ctc ccg tct ccc atc gag agg acc atc tct      1344
Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
            435                 440                 445

aag gcc aga ggg agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca      1392
Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
        450                 455                 460

tcc cca aag gag ttg tca tcc agt gac aca gtc agc atc acc tgc ctg      1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465                 470                 475                 480

ata aaa gac ttc tac cca cct gac att gat gtg gag tgg cag agc aat      1488
Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
                485                 490                 495

gga cag cag gag ccc gag agg aag cac cgc atg acc ccg ccc cag ctg      1536
Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu
                500                 505                 510

gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag      1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
            515                 520                 525

agc cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa      1632
Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
        530                 535                 540

act cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt      1680
Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545                 550                 555                 560

aaa tga                                                              1686
Lys
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<210> 72
<211> 561
<212> PRT
<213> Canis familiaris

78

<400> 72

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Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
  1               5                  10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
             20                  25                  30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35                  40                  45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
     50                  55                  60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65                  70                  75                  80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                 85                  90                  95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
             100                 105                 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
         115                 120                 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
     130                 135                 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
             165                 170                 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
         180                 185                 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
         195                 200                 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
     210                 215                 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
```

79

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290   295   300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
                325   330   335

Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
            340   345   350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
            355   360   365

Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
    370   375   380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385   390   395   400

Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
            405   410   415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
            420   425   430

Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
            435   440   445

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
    450   455   460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465   470   475   480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
            485   490   495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu

80

```
                  500                    505                      510

      Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
              515                  520                 525

      Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
          530                  535                 540

      Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
      545                  550                 555                 560

      Lys




      <210> 73
      <211> 1686
      <212> DNA
      <213> Canis familiaris

      <400> 73
      tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagtttcatg 60
      catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
      gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcct 180
      ctcgggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggtagaagtc 240
      ttttatcagg caggtgatgc tgactgtgtc actggatgac aactcctttg gggatggcgg 300
      caggacatac acactgggct tatgggccct ccctctggcc ttagagatgg tcctctcgat 360
      gggagacggg aggtctatgt ggttgactct gcacttgaac tccttccctg tgagccagtc 420
      ctggtgctca atggggagga cgctgaccac acggtaggtg ccgttgaact gctgctcacg 480
      agactgggtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
      agggtcctca cggcccagat ctaacaccac acaggtgacc tcgggtgttc gggtaatcct 600
      gaggatgtcc ttgggtttcg ggggaaagat gaggaccgaa ggccctccca gaggttcagg 660
      gactgggcat gggggtgtat cagtgcatct gcattcattg aacactggct tgtctacttt 720
      agtgttggat ccggtttcct tccagatatc acctttccag cattgttcat cactccactc 780
      actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840
      tttttggctt tcatttgatg ttcttgtgat ttgtatctca ttctcaactg tggtagtcac 900
      ccaagtagta ccatcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960
      tcctttaggc atgttccatt tcaggttaat ttcctctgaa ttcttcacag taagactaag 1020
      gtagtctggt ggcataggtt taactatatt ttgaagctga aaaataaaat agctgggtct 1080
      gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
      ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
      ctctgctgaa tggtccaagc cctcatacca gtaaacaac tggtaattgg tatcaaaatg 1260
      gacacccatg ccaggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
      catatcttga attttagttt cccgatttcc ttgtggtgat gtccaataag tagtttctgc 1380
      ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440
      tgcttcaata cctttgttaa gatcaaaccc atctttgtaa tgtagattct tggtaatgat 1500
      ggtcttccag ttttcactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560
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cttaaaatta tccggaaata atggaggttg ccattgcaaa gagagataac ctaaatatcc 1620
agggtccact atctcaaaat cctgaggagg attaactttt atctcagcat ttgaaagcat 1680
agacat                                                             1686


<210> 74
<211> 1698
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1695)

<400> 74
atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat      48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                  10                  15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg      96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                20                  25                  30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat     144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
            35                  40                  45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att     192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50                  55                  60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att     240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca     288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa     336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
                100                 105                 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac     384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115                 120                 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt     432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
```

82

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Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130                 135                 140


gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca     480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160


gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc     528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165                 170                 175


agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt     576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180                 185                 190


gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att     624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195                 200                 205


ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt     672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210                 215                 220


ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct     720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240


aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca     768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255


gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa     816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260                 265                 270


atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga     864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275                 280                 285


agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg     912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290                 295                 300


agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc     960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320


aac act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt    1008
```

83

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val
                  325   330   335

cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga   1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly
              340   345   350

ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctc ttg   1104
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu
          355   360   365

att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca   1152
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro
      370   375   380

gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg   1200
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met
385   390   395   400

caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac   1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
                  405   410   415

cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg   1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
              420   425   430

aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc   1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
          435   440   445

gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg   1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
      450   455   460

tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc   1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465   470   475   480

ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag   1488
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
                  485   490   495

tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc acg acc   1536
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
                  500   505   510

ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc   1584

84

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Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
        515                 520                 525

tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg      1632
Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
        530                 535                 540

gtg atg cat gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc      1680
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
545                 550                 555                 560

cat tct ccg ggt aaa tga                                              1698
His Ser Pro Gly Lys
                565


<210> 75
<211> 565
<212> PRT
<213> Canis familiaris

<400> 75
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                  10                  15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20                  25                  30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
        35                  40                  45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50                  55                  60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100                 105                 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
        115                 120                 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140
```

85

```
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145             150             155                 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165             170                 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180             185                 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195             200                 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210             215             220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225             230             235                 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
            245             250                 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
            260             265                 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
        275             280             285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
    290             295             300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305             310             315                 320

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val
            325             330                 335

Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly
            340             345                 350

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu
            355             360                 365

Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro
    370             375             380

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met
385             390             395                 400
```

86

Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
            405   410   415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
            420   425   430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
            435   440   445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
        450   455   460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465   470   475   480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
            485   490   495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
            500   505   510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
            515   520   525

Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
        530   535   540

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
545   550   555   560

His Ser Pro Gly Lys
                565

<210> 76
<211> 1698
<212> DNA
<213> Canis familiaris

<400> 76
tcatttaccc ggagaatggg agagggattc ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcaggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg agatggtcc tctcgatcgg 360

87

```
ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttccccttga gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagtgttgg atccggtttc cttccagata tcacctttcc agcattgttc 780
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 840
caaaaagcat aattttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 900
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 960
ggctggaatg ggtcctttag gcatgttcca tttcaggtta atttcctctg aattcttcac 1020
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 1080
atagctgggt ctgataggct gggattctga tgacccatta acacagatgt agaaatcttt 1140
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 1200
gtaatcagta cactctgctg aatggtccaa gccctcatac cagtaaaaca actggtaatt 1260
ggtatcaaaa tggacaccca tgccaggttt ccaagagcag actaaatatt gccagttgta 1320
atatacacag tccatatctt gaattttagt ttcccgattt ccttgtggtg atgtccaata 1380
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 1440
tgtgtttatc tttgcttcaa tacctttgtt aagatcaaac ccatctttgt aatgtagatt 1500
cttggtaatg atggtcttcc agttttcact atcaatgttt cggtatttta attcatattc 1560
tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1620
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1680
atttgaaagc atagacat                                              1698
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<210> 77
<211> 1692
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1689)

<400> 77
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atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat    48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                  10                  15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg    96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
             20                  25                  30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat   144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
         35                  40                  45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att   192
```

88

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att   240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca   288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa   336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac   384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt   432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca   480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc   528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165   170   175

agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt   576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180   185   190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att   624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195   200   205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt   672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct   720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca   768

89

```
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
            245                 250                 255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa    816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
            260                 265                 270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga    864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
            275                 280                 285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg    912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290                 295                 300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc    960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320

aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt   1008
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                325                 330                 335

aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct   1056
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
                340                 345                 350

tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc   1104
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
            355                 360                 365

cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac   1152
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
        370                 375                 380

cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca   1200
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
385                 390                 395                 400

gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg   1248
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
                405                 410                 415

gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag   1296
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
            420                 425                 430

ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag   1344
```

90

```
        Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
                435                 440                 445

        atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc      1392
        Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
                450                 455                 460

        ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc      1440
        Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
        465                 470                 475                 480

        tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag      1488
        Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
                        485                 490                 495

        agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc      1536
        Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
                500                 505                 510

        cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg      1584
        Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
                515                 520                 525

        gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg      1632
        Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
                530                 535                 540

        cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct      1680
        His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser
        545                 550                 555                 560

        ccg ggt aaa tga                                                      1692
        Pro Gly Lys


        <210> 78
        <211> 563
        <212> PRT
        <213> Canis familiaris

        <400> 78
        Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
         1               5                  10                  15

        Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                    20                  25                  30

        Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
```

91

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
            165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
            180   185   190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
            195   200   205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
    210   215   220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
            245   250   255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
            260   265   270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
    275   280   285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys
                        325   330   335

Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro
                        340   345   350

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala
                        355   360   365

Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn
        370   375   380

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr
385   390   395   400

Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val
                        405   410   415

Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln
                        420   425   430

Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu
                435   440   445

Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val
        450   455   460

Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr
465   470   475   480

Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln
                        485   490   495

Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro
                500   505   510

Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
                515   520   525

Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
        530   535   540

His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser

Pro Gly Lys

<210> 79
<211> 1692
<212> DNA
<213> Canis familiaris

<400> 79
tcatttaccc ggagaatggg agagggatat ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120
gctgtatagg aagtaggacc catcttcatc cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcag 300
gacatacaca ttaggctgat gggcctgccc tggggtcttg gagatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
gtgcccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgtc 720
tactttagtg ttggatccgg tttccttcca gatatcacct ttccagcatt gttcatcact 780
ccactcactc cagattccat catctgagca ataaatattc actttacttc ttaccaaaaa 840
gcataatttt tggctttcat ttgatgttct tgtgatttgt atctcattct caactgtggt 900
agtcacccaa gtagtaccat cctctgtgaa ttcaatttca taaatgaaac atttggctgg 960
aatgggtcct ttaggcatgt tccatttcag gttaatttcc tctgaattct tcacagtaag 1020
actaaggtag tctggtggca taggtttaac tatattttga agctgaaaaa taaaatagct 1080
gggtctgata ggctgggatt ctgatgaccc attaacacag atgtagaaat ctttatagtc 1140
tgatgactcc aaatagggaa acctgcatcc catatttttt ccattaacct tgatgtaatc 1200
agtacactct gctgaatggt ccaagccctc ataccagtaa aacaactggt aattggtatc 1260
aaaatggaca cccatgccag gtttccaaga gcagactaaa tattgccagt tgtaatatac 1320
acagtccata tcttgaattt tagtttcccg atttccttgt ggtgatgtcc aataagtagt 1380
ttctgcccat gaacttctaa cttctgatcc atttgtgcat tgtgctggca gaagtgtgtt 1440
tatctttgct tcaatacctt tgttaagatc aaacccatct ttgtaatgta gattcttggt 1500
aatgatggtc ttccagtttt cactatcaat gtttcggtat tttaattcat attctattgt 1560
gcattcctta aaattatccg gaaataatgg aggttgccat tgcaaagaga gataacctaa 1620
atatccaggg tccactatct caaaatcctg aggaggatta acttttatct cagcatttga 1680
aagcatagac at   1692

<210> 80
<211> 1686
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1683)

<400> 80
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atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat    48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1               5                  10                  15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg    96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
                20                  25                  30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat   144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
            35                  40                  45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att   192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
        50                  55                  60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att   240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65                  70                  75                  80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca   288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85                  90                  95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa   336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100                 105                 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac   384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
        115                 120                 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt   432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
        130                 135                 140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca   480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145                 150                 155                 160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc   528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
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95

agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt   576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
        180   185   190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att   624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195   200   205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt   672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210   215   220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct   720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225   230   235   240

aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca   768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245   250   255

gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa   816
Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
        260   265   270

atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga   864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
        275   280   285

agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg   912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290   295   300

agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc   960
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305   310   315   320

aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt   1008
Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys
                325   330   335

ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc   1056
Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe
                340   345   350

atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc   1104
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro

gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg   1152
Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
    370   375   380

cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg   1200
Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385   390   395   400

cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc   1248
Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                   405   410   415

ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc   1296
Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                   420   425   430

aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc   1344
Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
                   435   440   445

aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca   1392
Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
    450   455   460

tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg   1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465   470   475   480

atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag agc aat   1488
Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn
                   485   490   495

gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg   1536
Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu
                   500   505   510

gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag   1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
              515   520   525

agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg cat gaa   1632
Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu
    530   535   540

gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt   1680
Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly

97

aaa tga   1686
Lys

<210> 81
<211> 561
<212> PRT
<213> Canis familiaris

<400> 81
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp
 1   5   10   15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
            20   25   30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
        35   40   45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
    50   55   60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65   70   75   80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
                85   90   95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
            100   105   110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
            115   120   125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
    130   135   140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145   150   155   160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
                165   170   175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
                180   185   190

98

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Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
        195                 200                 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
        210                 215                 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225                 230                 235                 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
                245                 250                 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln
                260                 265                 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
        275                 280                 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
        290                 295                 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305                 310                 315                 320

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys
                325                 330                 335

Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe
                340                 345                 350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
                355                 360                 365

Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
        370                 375                 380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385                 390                 395                 400

Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                405                 410                 415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
                420                 425                 430

Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
        435                 440                 445
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99

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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
    450                 455                 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465                 470                 475                 480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn
                485                 490                 495

Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu
                500                 505                 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
            515                 520                 525

Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu
    530                 535                 540

Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545                 550                 555                 560

Lys
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<210> 82
<211> 1686
<212> DNA
<213> Canis familiaris

<400> 82
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catcaccgca catgtgaagg tgtctccctg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
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caggacatac acactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360
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gactgggcat ggggatatac acttgcaggt ggactctttg ggcactggct tgtctacttt 720
agtgttggat ccggtttcct tccagatatc acctttccag cattgttcat cactccactc 780
actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840
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ccaagtagta ccatcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960
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tcctttaggc atgttccatt tcaggttaat ttcctctgaa ttcttcacag taagactaag 1020
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gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140
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agacat   1686

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 9, 18, 21 and 27, n = unknown

<400> 83
athtggacnt ggaayccncc ngarggngc   29

<210> 84
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 6, 9, 21 and 33, n = unknown

<400> 84
atyttnccng crttrtcytt naccatdaty tgnac   35

<210> 85

101

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 12, 18 and 21, n = unknown

<400> 85
garathaarg tnaayccncc ncargaytty garat   35

<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 12, 22 and 31, n = unknown

<400> 86
tayaargayg gnttctgayy tnaayaargg nathga   36

<210> 87
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 7, 16, 25 and 40, n = unknown

<400> 87
ccaytcnswc cadatnccrt crtcngcrca rtadatrttn acytt   45

<210> 88

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<220>
<223> At locations 9 and 12, n = unknown

<400> 88
gcrtgrtcna rnccytcrta cca   23

<210> 89
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 89
agcggatccc tctatgcttt caaatgctga gataaaagtt aatcctcctc agg   53

<210> 90
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 90
tggacatcac cacaaggaaa tcggg   25

<210> 91
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 91
gcacatatgt ctatgctttc aaatgctgaa taaaagttaa tcctcctcag g   51

<210> 92
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 92
aaaggatccg gtttccttcc agatatcatt tccagc   36

<210> 93
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 93
ccgggatcca acactaaagt agacaagcgt g   31

<210> 94
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 94
gcgctcgagt catttacccg gagaatggga ggg   33

<210> 95
<211> 1525
<212> DNA

104

<213> Canis familiaris

<400> 95
gaattcggca cgagggagag gaggagggaa agatagaaag agagagagaa agattgcttg 60
ctacccctga acagtgacct ctctcaagac agtgctttgc tcttcacgta taaggaagga 120
aaacagtaga gattcaattt agtgtctaat gtggaaagga ggacaaagag gtcttgtgat 180
aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc tttcagcaca 240
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aagactataa ttactaggaa tctaatttac aaggatgggt ttgatcttaa taaaggcatt 540
gaaggaaaga tacgtacgca tttgtcagag cattgtacaa atggatcaga agtacaaagt 600
ccatggatag aagcttctta tgggatatca gatgaaggaa gtttggaaac taaaattcag 660
gacatgaagt gtatatatta taactggcag tatttggtct gctcttggaa acctggcaag 720
acagtatatt ctgataccaa ctataccatg ttttctggt atgagggctt ggatcatgcc 780
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ggagtcatat taaactcaat ttctcttaaa atttcgaata catcttcttg aaaatccaaa 1500
aaaaaaaaaa aaaaaaaaac tcgag 1525

<210> 96
<211> 1369
<212> DNA
<213> Canis familiaris

<400> 96
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ggcggggaga gaggcaatat caaggtttta aatctcggag aaatggcttt cgtttgcttg 120
gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac ttcatcttca 180
gacaccgaga taaaagttaa ccctcctcag gattttgaga tagtggatcc cggatactta 240
ggttatctct atttgcaatg gcaacccca ctgtctctgg tcatttaa ggaatgcaca 300
gtggaatatg aactaaaata ccgaaacatt ggtagtgaaa catggaagac catcattact 360
aagaatctac attacaaaga tgggtttgat cttaacaagg gcattgaagc gaagatacac 420
acgctttac catggcaatg cacaaatgga tcagaagttc aaagttcctg ggcagaaact 480
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tattacaatt ggcaatattt actctgttct tggaaacctg gcataggtgt acttcttgat 600
accaattaca acttgtttta ctggtatgag ggcttggatc atgcattaca gtgtgttgat 660

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<210> 97
<211> 1525
<212> DNA
<213> Canis familiaris

<400> 97
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aacagagggt atcttcataa gcacacactt ctttgttcag atccacatgg aggctcaatg 180
tgggttcagg ttcttccttc tccacaataa ggcaaagaag taacaaaagg aatataaaga 240
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aatctttata gtctgatgag tccaagttgg acagtttgca tccaacattt ttttcatcat 720
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gagagaggtc actgttcagg ggtagcaagc aatctttctc tctctctttc tatctttccc 1500
tcctcctctc cctcgtgccg aattc                                    1525
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                            106
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<210> 98
<211> 1369
<212> DNA
<213> Canis familiaris

<400> 98
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ttgaacattt ggccatgact ggaaactgtt gagtcaatac catgtctctt gatatggaaa 120
gtcttcatgt atcacagaaa aattctggaa tcatttttgg gtaggtgttt ggcttacgca 180
aaagcagacc ggttacaaat ataactaata ttaagatgaa accaaatggt agccagaaac 240
gtagcaaagt tttcttcgat aggtcttcac cttcccagca ttgtttatca ctccactcac 300
tccaaattcc gtcatctgag caataaatat tcactttgct tcttactaca aagcataatt 360
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aagccatttc tccgagattt aaaaccttga tattgcctct ctccccgccg acaggcacac 1320
ttctgaccag gttatggcga cttcaaatag ccttcatccg cgcggatcc   1369

<210> 99
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 99
ctctactatt ggcacagcag cctggga   27

<210> 100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 100
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<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 101
cctcccgagg gagccagccc g   21

<210> 102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 102
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<210> 103
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 103
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<210> 104
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Primer

<400> 104
ggtgagaata ccgaccccac g   21